

**Figure 1a****Variable Heavy Chain DNA****3077\_VH1B (SEQ ID NO: 1):**

```

(1)  CAGGTGCAAT TGGTTCAGAG CGGCGCGGAA GTGAAAAAAC CGGGCGCGAG
(51) CGTGAAAGTG AGCTGCAAAG CCTCCGATA TACCTTTACT TCTTATTCTA
(101) TTAATTGGGT CCGCCAAGCC CCTGGGCAGG GTCTCGAGTG GATGGGCTAT
(151) ATCGATCCGA ATCGTGGCAA TACGAATTAC GCGCAGAAGT TTCAGGGCCG
(201) GGTGACCATG ACCCGTGATA CCAGCATTAG CACCGCGTAT ATGGAAGTGA
(251) GCAGCCTGCG TAGCGAAGAT ACGGCCGTGT ATTATTGCGC GCGTGAGTAT
(301) ATTTATTTTA TTCATGGTAT GCTTGATTTT TGGGGCCAAG GCACCCTGTT
(351) GACGGTTAGC TCA

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**3079\_VH3 (SEQ ID NO: 2):**

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(1)  CAGGTGCAAT TGGTGGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
(51) CCTGCGTCTG AGCTGCGCGG CCTCCGATT TACCTTTTCT AATTATGGTA
(101) TGCATTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
(151) ATCCGTTCTG ATGGTAGCTG GACCTATTAT GCGGATAGCG TGAAAGGCCG
(201) TTTTACCATT TCACGTGATA ATTGCAAAAA CACCCTGTAT CTGCAAATGA
(251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTCGTTAT
(301) TGGTCTAAGT CTCATGCTTC TGTTACTGAT TATTGGGGCC AAGGCACCTT
(351) GGTGACGGTT AGCTCA

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**3080\_VH3 (SEQ ID NO: 3):**

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(1)  CAGGTGCAAT TGGTGGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
(51) CCTGCGTCTG AGCTGCGCGG CCTCCGATT TACCTTTTCT TCTTATGGTA
(101) TGCATTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
(151) ATCTATTCTG ATGGTAGCAA TACCTTTTAT GCGGATAGCG TGAAAGGCCG
(201) TTTTACCATT TCACGTGATA ATTGCAAAAA CACCCTGTAT CTGCAAATGA
(251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTAATATG
(301) TATCGTTGGC CTTTTCATTA TTTTTTTGAT TATTGGGGCC AAGGCACCTT
(351) GGTGACGGTT AGCTCA

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**3100\_VH 3 (SEQ ID NO: 4):**

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(1)  CAGGTGCAAT TGGTGGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
(51) CCTGCGTCTG AGCTGCGCGG CCTCCGATT TACCTTTTCT TCTAATGGTA
(101) TGTCTTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
(151) ATCTCTTATC TTTCTAGCTC TACCTATTAT GCGGATAGCG TGAAAGGCCG
(201) TTTTACCATT TCACGTGATA ATTGCAAAAA CACCCTGTAT CTGCAAATGA
(251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTTTTTAT
(301) GGTTATTTTA ATTATGCTGA TGTTTGGGGC CAAGGCACCC TGGTGACGGT
(351) TAGCTCA

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**3077\_1\_VH1B (SEQ ID NO: 31):**

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(1)  CAGGTGCAAT TAGTCCAAAG TGGTGCAGAA GTGAAAAAAC CGGGCGCGAG
(51) CGTGAAAGTG AGCTGCAAAG CCTCCGATA TACCTTTACT TCTTATTCTA

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(101) TTAATTGGGT CCGCCAAGCC CCTGGGCAGG GTCTCGAGTG GATGGGCTAT  
(151) ATCGATCCGA ATCGTGGCAA TACGAATTAC GCGCAGAAGT TTCAGGGCCG  
(201) GGTGACCATG ACCCGTGATA CCAGCATTAG CACCGCGTAT ATGGAAGTGA  
(251) GCAGCCTGCG TAGCGAAGAT ACGGCCGTGT ATTATTGCGC GCGTGAGTAT  
(301) ATTTATTTTA TTCATGGTAT GCTTGATTTT TGGGGCCAAG GCACCCTGGT  
(351) GACGGTTAGC TCA

**Figure 1b****Variable Heavy Chain Peptide**(CDR Regions in **Bold**)**3077\_VH1B (SEQ ID NO: 5):**

(1) QVQLVQSGAE VKKPGASVKV SCKAS**GYTFT** **SYSINWVRQA** PGQGLEWMGY  
(51) **IDPNRGNTNY** **AQKFQGRVTM** TRDTSISTAY MELSSLRSED TAVYYCAREY  
(101) **IYFIHGMLDF** WGQGTILVTVS S

**3079\_VH3 (SEQ ID NO: 6):**

(1) QVQLVESGGG LVQPGGSLRL SCAAS**GFTFS** **NYGMHWVRQA** PGKGLEWVSN  
(51) **IRSDGSWTTY** **ADSVKGRFTI** SRDNSKNTLY LQMNSLRAED TAVYYCARRY  
(101) **WSKSHASVTD** YWGQGTILVTV SS

**3080\_VH3 (SEQ ID NO: 7):**

(1) QVQLVESGGG LVQPGGSLRL SCAAS**GFTFS** **SYGMHWVRQA** PGKGLEWVSN  
(51) **IYSDGSNTFY** **ADSVKGRFTI** SRDNSKNTLY LQMNSLRAED TAVYYCARNM  
(101) **YRWPFHYFFD** YWGQGTILVTV SS

**3100\_VH 3 (SEQ ID NO: 8):**

(1) QVQLVESGGG LVQPGGSLRL SCAAS**GFTFS** **SNGMSWVRQA** PGKGLEWVSN  
(51) **ISYLSSTYY** **ADSVKGRFTI** SRDNSKNTLY LQMNSLRAED TAVYYCARFY  
(101) **GYFNYADVWG** QGTILVTVSS

**Figure 2a****Variable Light Chain DNA****3077\_Vk kappa 2 (SEQ ID NO: 9):**

```
(1)  GATATCGTGA TGACCCAGAG CCCACTGAGC CTGCCAGTGA CTCCGGGCGA
(51) GCCTGCGAGC ATTAGCTGCA GAAGCAGCCA AAGCCTGCTT TTTATTGATG
(101) GCAATAATTA TCTGAATTGG TACCTTCAAA AACCAGGTCA AAGCCCGCAG
(151) CTATTAATTT ATCTTGGTTC TAATCGTGCC AGTGGGGTCC CGGATCGTTT
(201) TAGCGGCTCT GGATCCGGCA CCGATTTTAC CCTGAAAATT AGCCGTGTGG
(251) AAGCTGAAGA CGTGGGCGTG TATTATTGCC AGCAGTATTC TTCTAAGTCT
(301) GCTACCTTTG GCCAGGGTAC GAAAGTTGAA ATTAAACGTA CG
```

**3079\_Vk kappa 1 (SEQ ID NO: 10):**

```
(1)  GATATCCAGA TGACCCAGAG CCCGTCTAGC CTGAGCGCGA GCGTGGGTGA
(51) TCGTGTGACC ATTACCTGCA GAGCGAGCCA GGATATTTCT GCTTTTCTGA
(101) ATTGGTACCA GCAGAAACCA GGTAAAGCAC CGAAACTATT AATTTATAAG
(151) GTTCTAATT TGCAAAGCGG GGTCCCGTCC CGTTTTAGCG GCTCTGGATC
(201) CGGCACTGAT TTTACCTTGA CCATTAGCAG CCTGCAACCT GAAGACTTTG
(251) CGACTTATTA TTGCCAGCAG GCTTATTCTG GTTCTATTAC CTTTGGCCAG
(301) GGTACGAAAG TTGAAATTAA ACGTACG
```

**3080\_VI lambda 3 (SEQ ID NO: 11):**

```
(1)  GATATCGAAC TGACCCAGCC GCCTTCAGTG AGCGTTGCAC CAGGTCAGAC
(51) CGCGCGTATC TCGTGTAGCG GCGATAATAT TGGTAATAAG TATGTTTCTT
(101) GGTACCAGCA GAAACCCGGG CAGGCGCCAG TTGTTGTGAT TTATGGTGAT
(151) AATAATCGTC CCTCAGGCAT CCCGGAACGC TTTAGCGGAT CCAACAGCGG
(201) CAACACCGCG ACCCTGACCA TTAGCGGCAC TCAGGCGGAA GACGAAGCGG
(251) ATTATTATTG CTCTTCTTAT GATTCTTCTT ATTTTGTGTT TGGCGGCGGC
(301) ACGAAGTTAA CCGTTCTTGG CCAG
```

**3100\_VI lambda 3 (SEQ ID NO: 12):**

```
(1)  GATATCGAAC TGACCCAGCC GCCTTCAGTG AGCGTTGCAC CAGGTCAGAC
(51) CGCGCGTATC TCGTGTAGCG GCGATAATAT TGGTCATTAT TATGCTTCTT
(101) GGTACCAGCA GAAACCCGGG CAGGCGCCAG TTCTTGTGAT TTATCGTGAT
(151) AATGATCGTC CCTCAGGCAT CCCGGAACGC TTTAGCGGAT CCAACAGCGG
(201) CAACACCGCG ACCCTGACCA TTAGCGGCAC TCAGGCGGAA GACGAAGCGG
(251) ATTATTATTG CCAGTCTTAT GATTATCTTC ATGATTTTGT GTTTGGCGGC
(301) GGCACGAAGT TAACCGTTCT TGGCCAG
```

**Figure 2b****Variable Light Chain Peptide**(CDR Regions in **Bold**)**3077\_Vk kappa 2 (SEQ ID NO: 13):**

(1) DIVMTQSPLS LPVTPGEPAS ISCR**SSQSLL FIDGNNY**LNW YLQKPGQSPQ  
(51) LLI**YLG**SNRA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV **YYCQQYSSKS**  
(101) ATFGQGTKVE IKRT

**3079\_Vk kappa 1 (SEQ ID NO: 14):**

(1) DIQMTQSPSS LSASVGDRVIT ITCRAS**QDIS AFLN**WYQQKP GKAPKLLI**YK**  
(51) **VSNLQ**SGVPS RFSGSGSGTD FTLTISSLPQ EDFATYYC**QQ AYSGS**ITFGQ  
(101) GTKVEIKRT

**3080\_Vl lambda 3 (SEQ ID NO: 15):**

(1) DIELTQPPSV SVAPGQTARI SC**SGDNIGNK YVSWY**QQKPG QAPVVVIY**GD**  
(51) **NNRPS**GIPER FSGSNSGNTA TLTISGTQAE DEADYYC**SSY DSSYF**VFGGG  
(101) TKLTVLGQ

**3100\_Vl lambda 3 (SEQ ID NO: 16):**

(1) DIELTQPPSV SVAPGQTARI SC**SGDNIGHY YASWY**QQKPG QAPVLVIY**RD**  
(51) **NDRPS**GIPER FSGSNSGNTA TLTISGTQAE DEADYYC**QSY DYLHDF**VFGG  
(101) GTKLTVLGQ

**Figure 3****Variable Heavy Chain Consensus Sequences**(CDR Regions in **Bold**)**VH1B Consensus (SEQ ID NO: 17):**

(1) QVQLVQSGAE VKKPGASVKV SCKAS**GYTFT** **SYMHWVRQA** PGQGLEWMGW  
(51) **INPNSGGTNY** **AQKFQGRVTM** TRDTSISTAY MELSSLRSED TAVYYCAR**WG**  
(101) **GDGFYAMDYW** GQGTILVTVSS

**VH3 Consensus (SEQ ID NO: 18):**

(1) QVQLVESGGG LVQPGGSLRL SCAAS**GFTFS** **SYAMSWVRQA** PGKGLEWVSA  
(51) **ISGSGGSTYY** **ADSVKGRFTI** SRDNSKNTLY LQMNSLRAED TAVYYCAR**WG**  
(101) **GDGFYAMDYW** GQGTILVTVS S

**Figure 4****Variable Light Chain Consensus Sequences**(CDR Regions in **Bold**)**VL<sub>λ</sub>3 Consensus (SEQ ID NO: 19):**

(1) SYELTQPPSV SVAPGQTARI **SCSGDALGDK YASWYQQKPG** QAPVLVIYDD  
(51) **SDRPSGIPER** FSGSNSGNTA TLTISGTQAE DEADYYC**QQH YTT**PPVFGGG  
(101) TKLTVLG

**VL<sub>k</sub>1 Consensus (SEQ ID NO: 20):**

(1) DIQMTQSPSS LSASVGDRVIT ITCRAS**QGIS SYLAWYQQKP** GKAPKLLIYA  
(51) **ASSLQSGVPS** RFGSGSGTD FTLTISSLQP EDFATYYC**QQ HYT**TPPTFGQ  
(101) GTKVEIKR

**VL<sub>k</sub>2 Consensus (SEQ ID NO: 21):**

(1) DIVMTQSPLS LPVTPGEPAS ISCRSS**QSL**L HSNQYNYLDW YLQKPGQSPQ  
(51) LLIY**LGSNRA** SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYC**QQHYT**TP  
(101) PTFGQGTKVE IKR

**Figure 5****Peptide Sequence of CD38**

(SEQ ID NO: 22):

```
1      mancefspvs gdkpccrlsr raqlclglsi lvlilvvla vvvprwrqqw sgpgttkrpf
61      etvlarcvky teihpemrhv dcqsvdafk gafiskhpcn iteedyqplm klgtqtvpcn
121     killwsrikd lahqftqvqr dmftledtll gyladdltwc gefntskiny qscpdwrkdc
181     snnpvsfvfwk tvsrrfaaaa cdvvhvmlng srskifdkns tfgsvevhn1 qpekvtlea
241     wvihggreds rdlcqdptik elesiiskrn iqfsckniyr pdkflqcvkn pedssctsei
```



**Figure 6****Nucleotide Sequence of Chimeric OKT10****Heavy Chain (SEQ ID NO: 23):**

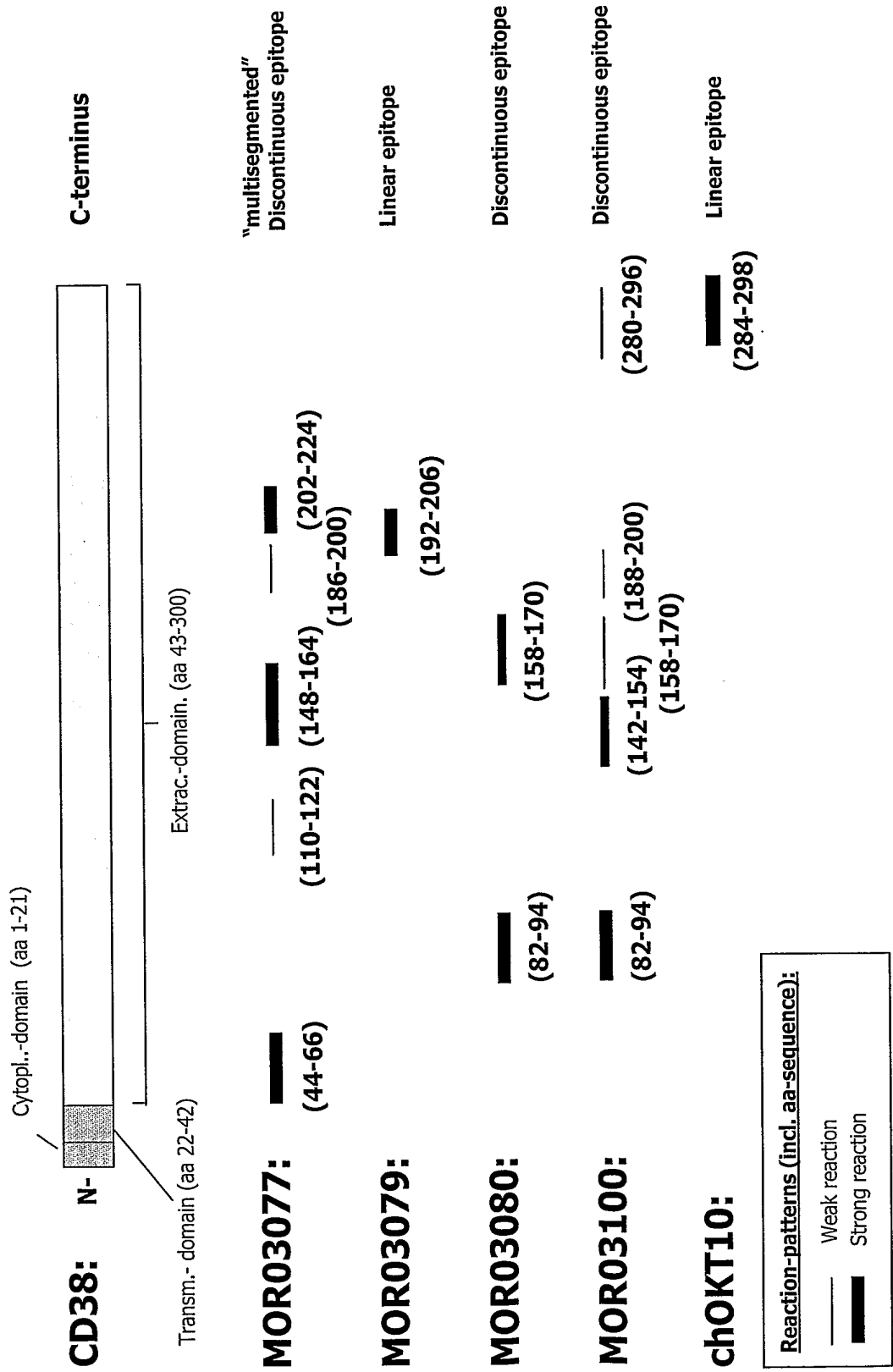
cagggtggaat tgggtggaatc tggaggatcc ctgaaactct cctgtgcagc ctcaggattc  
gatttttagta gatcctggat gaattgggtc cggcaggctc caggaaaagg gctagaatgg  
attggagaaa ttaatccaga tagcagtacg ataaactata cgacatctct aaaggataaa  
ttcatcatct ccagagacaa cgccaaaaat acgctgtacc tgcaaatgac caaagtgaga  
tctgaggaca cagcccttta ttactgtgca agatatggta actggtttcc ttattggggc  
caagggactc tggtcactgt cagctcagcc tccaccaagg gtccatcggc cttccccctg  
gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac  
tacttccccg aaccggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac  
accttccccg ctgtcctaca gtctcagga ctctactccc tcagcagcgt ggtgaccgtg  
ccctccagca gcttggggcac ccagacctac atctgcaacg tgaatcacia gccagcaac  
accaaggtgg acaagaaagt tgagcccaaa tcttgtgaca aaactcacac atgccaccg  
tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccc aaaaccaag  
gacaccctca tgatctcccc gaccctgag gtcacatgcg tggtggtgga cgtgagccac  
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaa  
acaaagccgc gggaggagca gtacaacagc acgtaccggg tggtcagcgt cctcacctgc  
ctgcaccagg actggctgaa tggcaaggag tacaagtgca aggtctccaa caaagccctc  
ccagccccc tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg  
tacaccctgc ccccatcccc ggatgagctg accaagaacc aggtcagcct gacctgctg  
gtcaaaggct tctatcccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag  
aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc  
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg  
catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaa

**Light Chain (SEQ ID NO: 24):**

gatatcctga tgaccagtc tcaaaaaatc atgccacat cagtgggaga cagggtcagc  
gtcacctgca aggccagtca aaatgtggat actaatgtag cctggatatca acagaaacca

ggacagtctc ctaaagcact gatttactcg gcacccctacc gatacagtgg agtccctgat  
cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcaccaa tgtgcagtct  
gaggacttgg cagagtatct ctgtcagcaa tatgacagct atcctctcac gttcgggtgct  
gggaccaagc tggacctgaa acgtacggtg gctgcacat ctgtcttcat cttcccgcca  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt

Fig.7: Schematic Overview of Epitopes



**Figure 8: DNA sequence of pMOPRH<sup>®</sup>\_h\_IgG1\_1**

```

                StyI
                ~~~~~
601   TCGCTATTAC CATGGTGATG CGGTTTTTGGC AGTACATCAA TGGGCGTGGA
      AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT ACCCGCACCT

                                           AatII
                                           ~~~~~
651   TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
      ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT

701   TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA
      ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT

751   ACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG
      TGTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC

801   GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
      CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTTGGGT GACGAATGAC

                pMORPH®_Ig_FOR 100.0%
                ~~~~~
851   GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
      CGAATAGCTT TAATTATGCT GAGTGATATC CCTCTGGGTT CGACCGATCG

                M K H L W F F L L L V A A P R
                ~~~~~
901   GCCACCATGA AACACCTGTG GTTCTTCCTC CTGCTGGTGG CAGCTCCCAG
      CGGTGGTACT TTGTGGACAC CAAGAAGGAG GACGACCACC GTCGAGGGTC

                EcoRI
                ~~~~~
                StyI
                ~~~~~
                BspI
                ~~~~~
                BlpI
                ~~~~~
                A S T

      · W V L S Q V E F C R R L A Q
951   ATGGGTCCTG TCCCAGGTGG AATTCTGCAG GCGGTTAGCT CAGCCTCCAC
      TACCCAGGAC AGGTCCACC TTAAGACGTC CGCCAATCGA GTCGAGGGTG

      StyI
      ~~~~~
      BbsI
      ~~~~~
      · K G P S V F P L A P S S K S T S G

1001  CAAGGGTCCA TCGGTCTTCC CCCTGGCACC CTCTCCAAG AGCACCTCTG
      GTTCCCAGGT AGCCAGAAGG GGGACCGTGG GAGGAGGTTT TCGTGGAGAC

      · G T A A L G C L V K D Y F P E P
1051  GGGGCACAGC GGCCCTGGGC TGCCTGGTCA AGGACTACTT CCCCGAACCG
      CCGGTGTGTC CCGGGACCCG ACGGACCAGT TCCTGATGAA GGGGCTTGGC

```

V T V S W N S G A L T S G V H T F  
 1101 GTGACGGTGT CGTGGAAGTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT  
 CACTGCCACA GCACCTTGAG TCCGCGGGAC TGGTCGCCGC ACGTGTGGAA  
 . P A V L Q S S G L Y S L S S V V T  
 1151 CCCGGCTGTC CTACAGTCCT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA  
 GGGCCGACAG GATGTCAGGA GTCCTGAGAT GAGGGAGTCG TCGCACCCT  
 . V P S S S L G T Q T Y I C N V N  
 1201 CCGTGCCCTC CAGCAGCTTG GGCACCCAGA CCTACATCTG CAACGTGAAT  
 GGCACGGGAG GTCGTCGAAC CCGTGGGTCT GGATGTAGAC GTTGCACTTA  
 StyI  
 ~~~~~  
 H K P S N T K V D K K V E P K S C  
 1251 CACAAGCCCA GCAACACCAA GGTGGACAAG AAAGTTGAGC CCAAATCTTG  
 GTGTTCCGGT CGTTGTGGTT CCACCTGTTC TTTCAACTCG GGTTTAGAAC  
 . D K T H T C P P C P A P E L L G G  
 1301 TGACAAAACCT CACACATGCC CACCGTGCCC AGCACCTGAA CTCCTGGGGG  
 ACTGTTTGA GTGTGTACGG GTGGCACGGG TCGTGGACTT GAGGACCCCC  
 BbsI StyI  
 ~~~~~ ~~~~~  
 . P S V F L F P P K P K D T L M I  
 1351 GACCGTCAGT CTTCTCTTTC CCCCCAAAC CCAAGGACAC CCTCATGATC  
 CTGGCAGTCA GAAGGAGAAG GGGGGTTTGT GGTTCCTGTG GGAGTACTAG  
 BbsI  
 ~~~~~  
 S R T P E V T C V V V D V S H E D  
 1401 TCCCGGACCC CTGAGGTCAC ATGCGTGGTG GTGGACGTGA GCCACGAAGA  
 AGGGCCTGGG GACTCCAGTG TACGCACCAC CACCTGCACT CGGTGCTTCT  
 BbsI  
 ~~~~~  
 . P E V K F N W Y V D G V E V H N A  
 1451 CCCTGAGGTC AAGTTCAACT GGTACGTGGA CGGCGTGGAG GTGCATAATG  
 GGGACTCCAG TTCAAGTTGA CCATGCACCT GCCGCACCTC CACGTATTAC  
 . K T K P R E E Q Y N S T Y R V V  
 1501 CCAAGACAAA GCCGCGGGAG GAGCAGTACA ACAGCACGTA CCGGGTGGTC  
 GTTCTGTTT CGGCGCCCTC CTCGTCATGT TGTCTGTCAT GGCCACCAG  
 S V L T V L H Q D W L N G K E Y K  
 1551 AGCGTCCTCA CCGTCCTGCA CCAGGACTGG CTGAATGGCA AGGAGTACAA  
 TCGCAGGAGT GGCAGGACGT GGTCTGACC GACTTACCGT TCCTCATGTT  
 . C K V S N K A L P A P I E K T I S  
 1601 GTGCAAGGTC TCCAACAAAG CCCTCCCAGC CCCCATCGAG AAAACCATCT  
 CACGTTCCAG AGGTTGTTTC GGGAGGGTCG GGGGTAGCTC TTTTGGTAGA

```

                                BsrGI
                                ~~~~~
1651  . K A K G Q P R E P Q V Y T L P P
      CCAAAGCCAA AGGGCAGCCC CGAGAACCAC AGGTGTACAC CCTGCCCCCA
      GGTTTCGGTT TCCCGTCGGG GCTCTTGGTG TCCACATGTG GGACGGGGGT

      S R D E L T K N Q V S L T C L V K

1701  TCCCGGGATG AGCTGACCAA GAACCAGGTC AGCCTGACCT GCCTGGTCAA
      AGGGCCCTAC TCGACTGGTT CTTGGTCCAG TCGGACTGGA CGGACCAGTT

      . G F Y P S D I A V E W E S N G Q P

1751  AGGCTTCTAT CCCAGCGACA TCGCCGTGGA GTGGGAGAGC AATGGGCAGC
      TCCGAAGATA GGGTCGCTGT AGCGGCACCT CACCCTCTCG TTACCCGTCG

      . E N N Y K T T P P V L D S D G S
1801  CGGAGAACAA CTACAAGACC ACGCCTCCCG TGCTGGACTC CGACGGCTCC
      GCCTCTTGTT GATGTTCTGG TCGGGAGGGC ACGACCTGAG GCTGCCGAGG

      F F L Y S K L T V D K S R W Q Q G

1851  TTCTTCCTCT ACAGCAAGCT CACCGTGGAC AAGAGCAGGT GGCAGCAGGG
      AAGAAGGAGA TGTCGTTCTGA GTGGCACCTG TTCTCGTCCA CCGTCGTCCC

      BbsI                      NsiI
      ~~~~~                      ~~~~~
      . N V F S C S V M H E A L H N H Y T

1901  GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCACTACA
      CTTGCAGAAG AGTACGAGGC ACTACGTACT CCGAGACGTG TTGGTGATGT

      SapI                      PmeI
      ~~~~~                      ~~~~~
      . Q K S L S L S P G K *
1951  CGCAGAAGAG CCTCTCCCTG TCTCCGGGTA AATGAGGGCC CGTTTAAACC
      GCGTCTTCTC GGAGAGGGAC AGAGGCCCAT TTACTCCCGG GCAAATTTGG

2001  CGCTGATCAG CCTCGACTGT GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG
      GCGACTAGTC GGAGCTGACA CGGAAGATCA ACGGTCGGTA GACAACAAAC

      ~~~~~
2051  pMORPH®_Ig_REV 100.0%
      CCCCTCCCCC GTGCCTTCCT TGACCCTGGA AGGTGCCACT CCCACTGTCC
      GGGGAGGGGG CACGGAAGGA ACTGGGACCT TCCACGGTGA GGGTGACAGG

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|      |                                   |                                  |             |            |             |  |  |  |  |  |  |       |  |
|------|-----------------------------------|----------------------------------|-------------|------------|-------------|--|--|--|--|--|--|-------|--|
|      |                                   | StyI                             |             |            |             |  |  |  |  |  |  |       |  |
|      |                                   | ~~~~~                            |             |            |             |  |  |  |  |  |  |       |  |
| 601  | TCGCTATTAC                        | CATGGTGATG                       | CGGTTTTGGC  | AGTACATCAA | TGGGCGTGGA  |  |  |  |  |  |  |       |  |
|      | AGCGATAATG                        | GTACCACTAC                       | GCCAAAACCG  | TCATGTAGTT | ACCCGCACCT  |  |  |  |  |  |  |       |  |
| 651  | TAGCGGTTTG                        | ACTCACGGGG                       | ATTTCCAAGT  | CTCCACCCCA | TTGACGTCAA  |  |  |  |  |  |  |       |  |
|      | ATCGCCAAAC                        | TGAGTGCCCC                       | TAAAGGTTCA  | GAGGTGGGGT | AACTGCAGTT  |  |  |  |  |  |  |       |  |
| 701  | TGGGAGTTTG                        | TTTGTGCACC                       | AAAATCAACG  | GGACTTTCCA | AAATGTCGTA  |  |  |  |  |  |  |       |  |
|      | ACCCTCAAAC                        | AAAACCGTGG                       | TTTTAGTTGC  | CCTGAAAGGT | TTTACAGCAT  |  |  |  |  |  |  |       |  |
| 751  | ACAACTCCGC                        | CCCATTGACG                       | CAAATGGGCG  | GTAGGCGTGT | ACGGTGGGAG  |  |  |  |  |  |  |       |  |
|      | TGTTGAGGCG                        | GGGTAAC TGC                      | GT'TTACCCGC | CATCCGCACA | TGCCACCCTC  |  |  |  |  |  |  |       |  |
| 801  | GTCTATATAA                        | GCAGAGCTCT                       | CTGGCTAACT  | AGAGAACCCA | CTGCTTACTG  |  |  |  |  |  |  |       |  |
|      | CAGATATATT                        | CGTCTCGAGA                       | GACCGATTGA  | TCTCTTGGGT | GACGAATGAC  |  |  |  |  |  |  |       |  |
|      |                                   | pMORPH <sup>®</sup> _Ig_FOR 100% |             |            |             |  |  |  |  |  |  | NheI  |  |
|      |                                   | =====                            |             |            |             |  |  |  |  |  |  | ~~~~~ |  |
| 851  | GCTTATCGAA                        | ATTAATACGA                       | CTCACTATAG  | GGAGACCCAA | GCTGGCTAGC  |  |  |  |  |  |  |       |  |
|      | CGAATAGCTT                        | TAAT'TATGCT                      | GAGTGATATC  | CCTCTGGGTT | CGACCGATCG  |  |  |  |  |  |  |       |  |
| +1   |                                   | M V L Q T Q V F I S L L L W I    |             |            |             |  |  |  |  |  |  |       |  |
|      |                                   | StyI                             |             |            |             |  |  |  |  |  |  |       |  |
|      |                                   | ~~~~~                            |             |            |             |  |  |  |  |  |  |       |  |
| 901  | GCCACCATGG                        | TGTTGCAGAC                       | CCAGGTCTTC  | ATTTCTCTGT | TGCTCTGGAT  |  |  |  |  |  |  |       |  |
|      | CGGTGGTACC                        | ACAACGTCTG                       | GGTCCAGAAG  | TAAAGAGACA | ACGAGACCTA  |  |  |  |  |  |  |       |  |
|      |                                   |                                  | BbsI        |            |             |  |  |  |  |  |  |       |  |
|      |                                   |                                  | ~~~~~       |            |             |  |  |  |  |  |  |       |  |
| +1   | S G A Y G D I V M I K R T V A A   |                                  |             |            |             |  |  |  |  |  |  |       |  |
|      |                                   | EcoRV                            |             |            |             |  |  |  |  |  |  | BsiWI |  |
|      |                                   | ~~~~~                            |             |            |             |  |  |  |  |  |  | ~~~~~ |  |
| 951  | CTCTGGTGCC                        | TACGGGGGATA                      | TCGTGATGAT  | TAAACGTACG | GTGGCTGCAC  |  |  |  |  |  |  |       |  |
|      | GAGACCACGG                        | ATGCCCTTAT                       | AGCACTACTA  | ATTTGCATGC | CACCGACGTG  |  |  |  |  |  |  |       |  |
| +1   | P S V F I F P P S D E Q L K S G T |                                  |             |            |             |  |  |  |  |  |  |       |  |
| 1001 | CATCTGTCTT                        | CATCTTCCCG                       | CCATCTGATG  | AGCAGTTGAA | ATCTGGAAC T |  |  |  |  |  |  |       |  |
|      | GTAGACAGAA                        | GTAGAAGGGC                       | GGTAGACTAC  | TCGTCAACTT | TAGACC'TTGA |  |  |  |  |  |  |       |  |
|      |                                   | BbsI                             |             |            |             |  |  |  |  |  |  |       |  |
|      |                                   | ~~~~~                            |             |            |             |  |  |  |  |  |  |       |  |

```

+1  A S V V C L L N N F Y P R E A K V
1051 GCCTCTGTTG TGTGCCTGCT GAATAACTTC TATCCCAGAG AGGCCAAAGT
    CCGAGACAAC ACACGGACGA CTTATTGAAG ATAGGGTCTC TCCGGTTTCA

+1  Q W K V D N A L Q S G N S Q E S
1101 ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC CAGGAGAGTG
    TGTACCTTC CACCTATTGC GGGAGGTTAG CCCATTGAGG GTCCTCTCAC

+1  V T E Q D S K D S T Y S L S S T L
1151 TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCTTG
    AGTGTCCTCGT CCTGTCGTTT CTGTCGTGGA TGTGCGAGTC GTCGTGGGAC

+1  T L S K A D Y E K H K V Y A C E V
    BlpI
    ~~~~~
1201 ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT
    TGC GACTCGT TTCGTCTGAT GCTCTTTGTG TTTCAGATGC GGACGCTTCA

+1  T H Q G L S S P V T K S F N R G
1251 CACCCATCAG GGCCTGAGCT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG
    GTGGGTAGTC CCGGACTCGA GCGGGCAGTG TTTCTCGAAG TTGTCCCCTC

+1  E C *
                                PmeI
                                ~~~~~
                                pMORPH®_Ig_REV 100%
                                =====
1301 AGTGTTAGGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT
    TCACAATCCC CGGGCAAATT TGGGCGACTA GTCGGAGCTG ACACGGAAGA

=
1351 AGTTGCCAGC CATCTGTTGT TTGCCCCCTCC CCCGTGCCTT CCTTGACCCT
    TCAACGGTCG GTAGACAACA AACGGGGAGG GGGCACGGAA GGAAGTGGGA

```



**Figure 10: DNA Sequence of HuCAL<sup>®</sup> Ig lambda light chain vector**  
**pMORPH<sup>®</sup>\_h\_Igλ\_1**

```

                StyI
                ~~~~~~
601  TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA
    AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT ACCCGCACCT

651  TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
    ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT

701  TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA
    ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT

751  ACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG
    TGTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC

801  GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
    CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTTGGGT GACGAATGAC

                pM_Ig_FOR 100.0%
                =====
                NheI
                ~~~~~~
851  GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
    CGAATAGCTT TAATTATGCT GAGTGATATC CCTCTGGGTT CGACCGATCG

+1      M A W A L L L L T L L T Q G T
        StyI
        ~~~~~~
901  GCCACCATGG CCTGGGCTCT GCTGCTCCTC ACCCTCCTCA CTCAGGGCAC
    CCGTGGTACC GGACCCGAGA CGACGAGGAG TGGGAGGAGT GAGTCCCGTG

+2      T V L G Q
+1      G S W A D I V M H E V
        BamHI      EcoRV      HpaI      StyI
        ~~~~~~      ~~~~~~      ~~~~~~      ~~~~~~
951  AGGATCCTGG GCTGATATCG TGATGCACGA AGTTAACCGT CCTAGGTCAG
    TCCTAGGACC CGACTATAGC ACTACGTGCT TCAATTGGCA GGATCCAGTC

+2      P K A A P S V T L F P P S S E E L
        StyI
        ~~~~~~
1001  CCCAAGGCTG CCCCCTCGGT CACTCTGTTC CCGCCCTCCT CTGAGGAGCT
    GGGTTCCGAC GGGGGAGCCA GTGAGACAAG GCGGGGAGGA GACTCCTCGA

+2      Q A N K A T L V C L I S D F Y P
1051  TCAAGCCAAC AAGGCCACAC TGGTGTGTCT CATAAGTGAC TTCTACCCGG
    AGTTCGGTTG TTCCGGTGTG ACCACACAGA GTATTCAGT AAGATGGGCC

```

+2 G A V T V A W K G D S S P V K A G  
1101 GAGCCGTGAC AGTGGCCTGG AAGGGAGATA GCAGCCCCGT CAAGGCGGGA  
CTCGGCACTG TCACCGGACC TTCCCTCTAT CGTCGGGGCA GTTCCGCCCT

+2 V E T T T P S K Q S N N K Y A A S  
1151 GTGGAGACCA CCACACCCTC CAAACAAAGC AACAAACAAGT ACGCGGCCAG  
CACCTCTGGT GGTGTGGGAG GTTTGTTTCG TTGTTGTTCA TGCGCCGGTC

+2 S Y L S L T P E Q W K S H R S Y  
1201 CAGCTATCTG AGCCTGACGC CTGAGCAGTG GAAGTCCCAC AGAAGCTACA  
GTCGATAGAC TCGGACTGCG GACTCGTCAC CTTCAGGGTG TCTTCGATGT

+2 S C Q V T H E G S T V E K T V A P  
BbsI  
~~~~~  
1251 GCTGCCAGGT CACGCATGAA GGGAGCACCG TGGAGAAGAC AGTGGCCCCCT  
CGACGGTCCA GTGCGTACTT CCCTCGTGGC ACCTCTTCTG TCACCGGGGA

+2 T E C S \*  
PmeI  
~~~~~  
1301 ACAGAATGTT CATAGGGGCC CGTTTAAACC CGCTGATCAG CCTCGACTGT  
TGTCTTACAA GTATCCCCGG GCAAATTTGG GCGACTAGTC GGAGCTGACA  
pM\_Ig\_REV 100%  
=====

1351 GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG CCCCTCCCCC GTGCCTTCCT  
CGGAAGATCA ACGGTCGGTA GACAACAAAC GGGGAGGGGG CACGGAAGGA  
pM\_Ig\_REV 100.0%  
=====



Fig. 12: IL-6 Release Assay

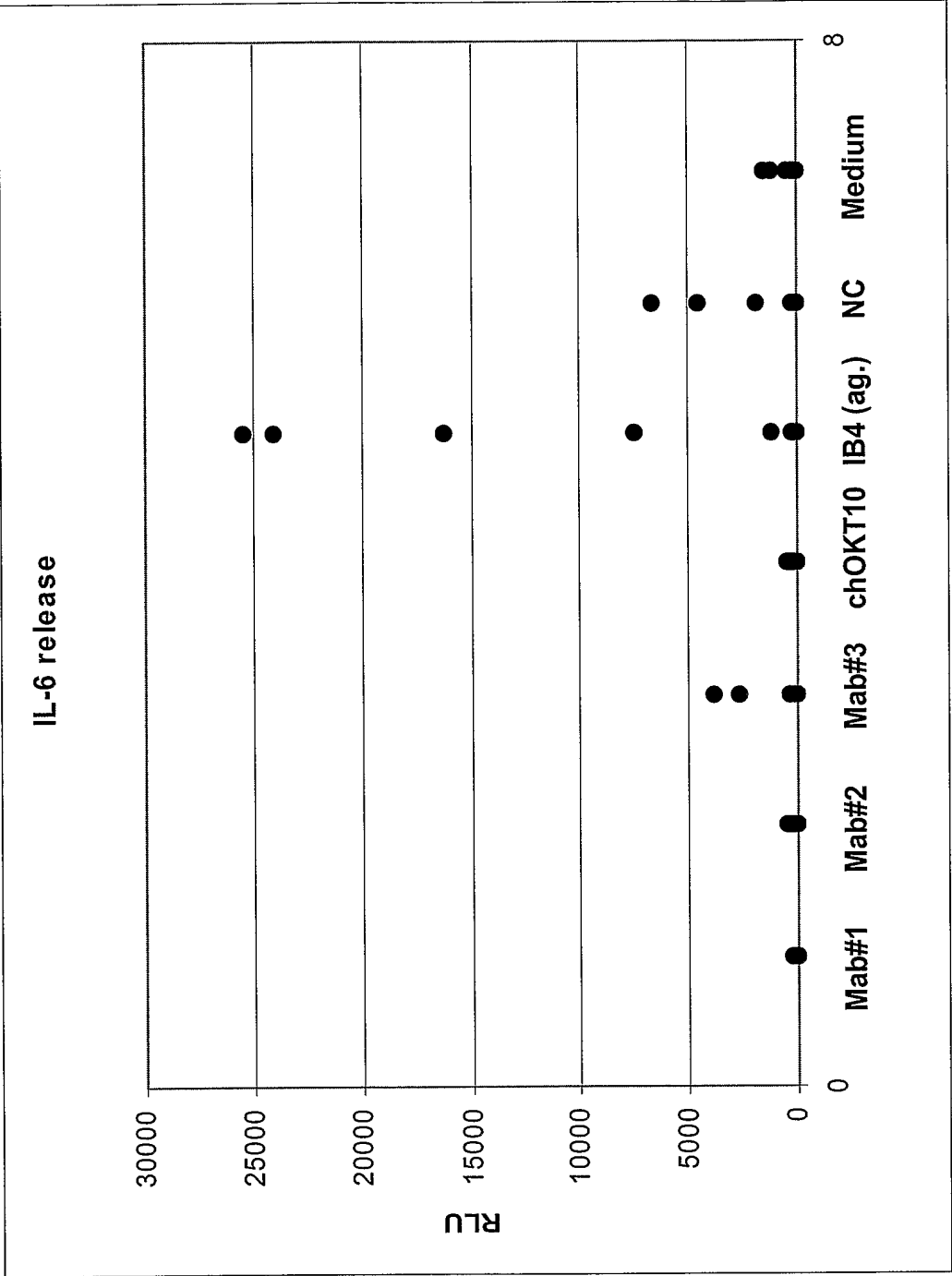


Fig. 13: Cytotoxicity towards CD34+/CD38+ progenitor cells

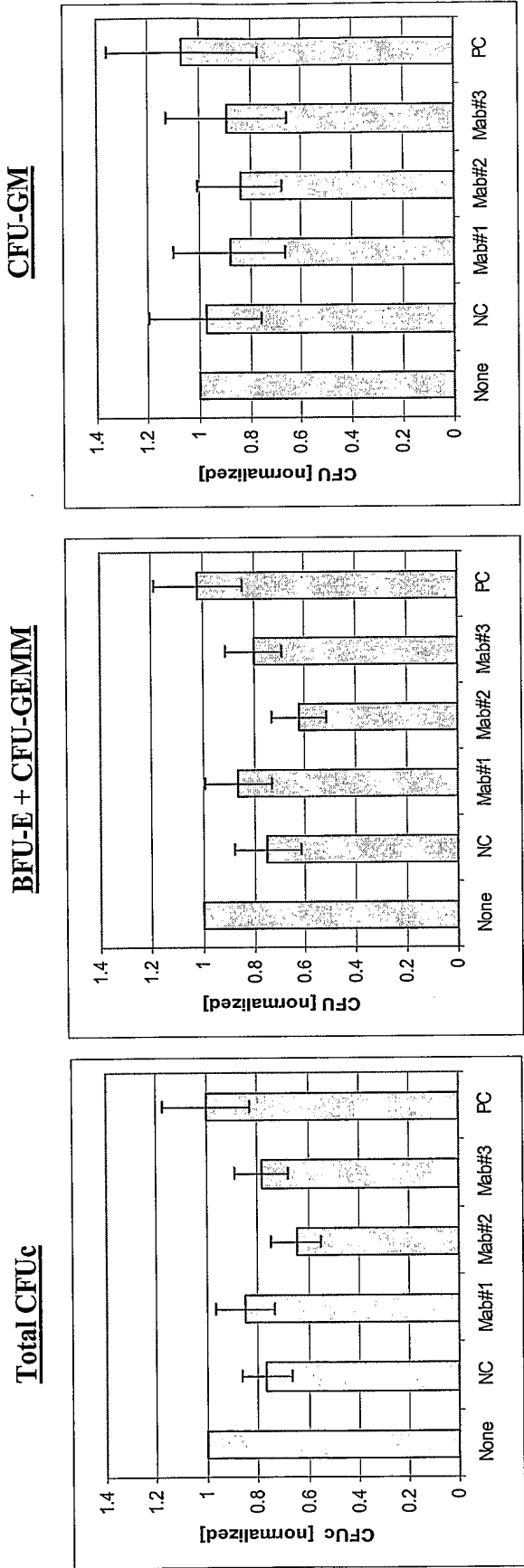


Fig. 14: ADCC with different cell-lines

| Cell line          | Culture Collection                      | Origin           | Expression<br>[MFI] | Max. specific killing [%] in ADCC <sup>a,c</sup> |       |       |      |
|--------------------|---|------------------|---------------------|--|-------|-------|------|
|                    |   |                  |                     | Mab#1  | Mab#2 | Mab#3 | PC   |
| RPMI 8226          | ATCC CCL-155                            | MM               | 405.71              | 56   | 58    | 54    | 46   |
| KMS-12-BM          | DSMZ ACC551                             | MM               | 142.29              | 26   | 32    | 30    | 34   |
| NCI-H929           | ECACC95050415                           | MM               | 45.01               | 68   | 73    | 38    | 54   |
| OPM-2              | DSMZ ACC50                              | MM               | 37.99               | 6  | 13    | 3     | 7    |
| U-266              | ECACC85051003                           | MM               | 26.14               | 17   | 14    | 12    | 16   |
| KMS-11             | Namba <i>et al.</i> , 1989 <sup>b</sup> | MM               | 26.81 <sup>d</sup>  | 22   | 30    | 26    | 28   |
| JVM-13             | DSMZACC19                               | CLL              | 463.93              | 11   | 20    | 12    | 15   |
| JVM-2              | DSMZACC12                               | CLL              | 140.84              | 22   | 28    | 10    | 24   |
| CCRF-CEM           | ECACC85112105                           | ALL              | 301.46              | 24   | 29    | 20    | 22   |
| Jurkat             | DSMZ ACC282                             | ALL              | 202.99              | 7  | 8     | 13    | 12   |
| AML-193            | DSMZ ACC549                             | AML              | 62.69 <sup>d</sup>  | 33   | 26    | 39    | 33   |
| OCI-AML5           | DSMZ ACC247                             | AML              | 207.55 <sup>d</sup> | 20   | 21    | 16    | 26   |
| NB-4               | DSMZ ACC207                             | AML              | 164.7 <sup>d</sup>  | 36   | 38    | 32    | 37   |
| THP-1              | DSMZ ACC16                              | AML              | 34.41               | 64   | 59    | 38    | 43   |
| HL-60 <sup>d</sup> | DSMZ ACC3                               | AML              | 18.43 <sup>d</sup>  | 29   | 35    | 29    | 29   |
| Raji               | Burkitt's Lymph.                        | Burkitt's lymph. | n.d.                | 53   | 62    | 48    | n.d. |

Fig. 15: ADCC with MM-samples

| Antibodies                           |  | Mab#1       | Mab#2       | Mab#3       | PC          |
|--------------------------------------|--|-------------|-------------|-------------|-------------|
| Parameters:                          |  |             |             |             |             |
| MM samples: EC50 [nM] <sup>a</sup> : |  | 0.116-0.202 | 0.006-0.185 | 0.027-0.249 | 0.282-0.356 |
| MM samples: Max spec. killing [%]    |  | 13.1 - 61.6 | 16.2 - 57.9 | 13.6 - 36.0 | 15.5 - 49.5 |

Fig. 16: Treatment of human myeloma xenograft with MOR03080

